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FIG. 1

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302 TCGGCGCTCACAACCTGCCCCCGAACCAAGGCTGCCCAGCACCCCTCCCGCT 351
||| :::||||| ||| |||:::
810 CysGluLysValThrCysProProLeuThrCysSerArgProIleArgAr 826

352 G...CCAGACTCCTGCTGCCAAGCCTGCAAGATGAGGCAAGTGAGCAAT 398
|||:~::~:|||||:: ||| ||| :~::~
826 gAsnProSerAspCysCysLysGluCysProProGluGluThrProProL 843

399 CGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAG 448
:~::~:|||||:: :~::~:|||||:::
843 euGluAspGluGluMetMetGlnAla..... 851

449 GATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCCGCAGC 498
|||||
852AspGlyThr..... 854

499 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 548

854 854

549 CCAAGGGAGCAGGCACAACTGTCAAGATCGTCCTGAAGGAGAAACAT 598

854 854

FIG. 1 (CONT.¹)

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```
863 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 912
    ||| ||| ::::: ||| ::|
3 SerTyrHisArgSerHisTyrAspProProSerArgGlnAlaGlyG1 19

913 GAGAAAGAGAGGCGCGGCCACCCAGCCCCCAGCTGGCCTCAGCGCCCTC 962
    | ::||| |||||::: ::|
19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

963 TGAGCTTCATCCCTCGCCACTTCAGACCCCAAGGGAGCAGGCAGCAACT 1012
    ::| ::| ::| ::| ::|
34 .....MetAspSerGlnGlnAlaSerGlyThrIle 43

1013 GTCAAGATCGTCCCTG.....AAGGAGAAACATANGAAAGCCTGTGTGCA 1056
    |||:::|||||::: |||:::||||| :::::|||||
44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60

1057 TGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTG 1106
    :::||||| ||||| ||||| ||||| ||||| ::|
60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArga 77

1107 CCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCCAG 1156
    ||||| |||:::||||| ||||| ::|
77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93
```

FIG.2A

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```

1157 GACTGCCAGCGTGTGACCTGTCCACGAAGTACCCCTGCCGTACCCCCGA 1206
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
94  GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGlu 110

1207 GAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGGACAAAGCAGAC. 1255
      ::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
110  nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1256 .....CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1294
      |||||:::  :::::  :::::  :::::  |||  :::
127  luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1295 GCACCGGGCGGGTCCCTCGTCCACACATCGGTA...TCCCCAAGCCCCAGA 1341
      ::  ||:::  |||||  :::  :::  :::
144  Glu.....ThrMetProValTyrGluSerValPheMetGluAspGlyGlu 158

1342 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCCTCGGACTTGGTGGAGA 1391
      :::  ||:::  :::  |||||  |||  |||||
158  uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1392 TCTACCTCTGGAAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNN 1441
      :::::  |||  :::
175  alHisValTrpThrIle..... 180

```

FIG.2A (CONT.)

[illegible]

FIG.2A (CONT.)²⁾

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100 TCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCTGCCCCACCGCTG 149
 :::||||| ||| ||::: ||::: |||
429 ThrAlaHisLeuLeuGlyPro.....ProGlyThrProGlyProArg.. 442

150 CTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGACACCTCCTGGGTCA 199
 ||||::: :::||||: |||||:
443ArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyValV 457

200 TGTGGGTTGATCTGTGGCCCTGTGNCCTCCGTGTCCTTTTCGTCTCCCGT 249
 :: ||||| ||| ||||| |||
457 al...LysAspLeuGluProGluLeuLeuArgHisLeu..... 468

250 CCTCCGACTCCGCTCCCGACACGCGGCTGACCCCTGGGAAAGGATGG 299
 ||| ||| ||:::++
469AlaLysGlyMetAlaSerLeuLeuIleThrThrLysGl 481

300 TTCC...CGAGGTGAG..... 312
 ||| |||||
481 ySerProArgGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysG 498

FIG. 2B

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313GGTCCTCTCCTCCTT.....GCTGGGACTCGCGCT 342
||| ||| ||| |||:::|||||
498 luValGlyGlyLeuArgLeuAlaAlaGlyAlaGluGlyValArgAla 514

342 342
515 LeuGlyAlaProAspProAlaSerAlaAlaProProValValProGlyLe 531
343GCTCTGGTTCCC.....CCTGGACTCCCACGCTCGAGCCCGCCCA 382
|||||:::|||| | |||:::|||| |
531 uProAlaLeuAlaProAlaLysProGlyGlyPro.GlyArgProArgAsp 547
383 GACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGAGAGCTG 432
|||:::||||:::|||| | ||| |
548 ProAsnThrCysPheGluGlyGlnGlnArgProHisGlyAlaArgTr 564
433 GCACCCCTACTTGGAGCCACAAAGGCCTGATGTACTGCCCTGGCTGTACCT 482
| ||| :::|| | ||| |
564 pAlaProAsnTyrAspPro.....LeuCysSerLeuCysThrC 577

FIG. 2B (CONT.)

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[illegible]FIG. 2B (CONT.²)

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```

756 CCTGCCCCGAACCAAGGCTGCCCCAGCAGCCCTCCCGCTG...CCAGACTCC 802
      |||||::: ::::||| |||::: ::: ||| :::
675 lnCysProArgLeuAlaCysAlaGlnProValArgValAsnProThrAsp 691
803 TGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGA 852
      |||||::: |||
692 CysCysLysGlnCys..... 696
853 CAGTGTGCAGTCGCTCCATGGGTGAGACATCCTCAG.....GATCCAT 896
      ::: ::: ||||| |||||
697 .....ProValGlySerGlyAlaHisProGlnLeuGlyAspProm 710
897 GTTCCAGTGATGCTGGGAGAAAGAGAGAGGCCCGGCACCCAGCCCCCCT 946
      :::::||| |||||
710 etGlnAlaAsp.....GlyPro..... 715
947 GGCTCAGCGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCCAAGGG 996
715 ..... 715
997 AGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATANGAAAG 1046
      :::
716 .....ArgG 717

```

FIG. 2B (CONT.)³⁾

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```
1047 CCTGTGTCATGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCG 1096
      ::||| ::|||::: ::: :::::~::~ |||||~|||
717 lYcysArgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisPro 733

1097 GCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCTGTGAGGA 1146
      ::: ||||| ||||| ||||| ||| |||
734 SerValProProPheGlyGluMetSerCysIleThrCysArgCysGlyAl 750

1147 TGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCC 1196
      ||| |||:::~||| ||| |||
750 aGlyValProHisCysGluArgAspAspCysSerLeuProLeuSerCysG 767

1197 GTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTC..... 1237
      :::::~: :::::~|||~|::: |||
767 lYSerGlyLysGlu:.....SerArgCysCysSerArgCysThrAlaHis 781

1238 .....~.....CCAGAGGACAAAGCAGACCCCT 1258
      ||||| :::::~|||~|
782 ArgArgProAlaProGluThrArgThrAspPro 792
```

FIG. 2B (CONT.)

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```

3  CTTCCCCCTTCTTTGATCGCCTCTCC.....CTTCTGCTGGA 40
   |||||  ::::  |||  |||||
540 LeuProValArgSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 556

41 CCTTCCTTCGTCCTCTCCATCTCTCCCTCCTT.....T 72
   |  |||||  ::::  |||
556 pThrHisCysHisLeuHisTyrGluValLeuAlaGlyLeuGlyGlys 573

73 CCCCCGCTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTT 122
   ||  ::::  |||  +++
573 erGluGlnGlyThrValThr..... 579

123 CCTGCCCTCCTTCTCTGCCACCGCTGCTTCTGCGCCCTTCTCCGACCCC 172
   |||  |||  |||||  ::|||  |||  ::|||
580 ...AlaHisLeuLeuGlyProProGlyMetProGlyProGln.ArgLeuL 595

173 GCTCT.....AGCAGCAGACCTCCTGGGGTCATGTGGGTTGATCTG 213
   ::  ::|||  ::|||  ::|||  ::|||
595 euLysGlyPheTyrGlySerGluAlaGlnGlyValVal...LysAspLeu 610

214 TGGCCCCCTGTGNCTCCGT.....GT 233
   |||  ::|||  ::
611 GluProValLeuLeuArgHisLeuAlaGlnGlyThrAlaSerLeuLeuI 627

```

Fig. 2C

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```

234 CCTTTTCGTCTCCCGTCTCCCGACTCCGCTCCCGGACCA..... 273
      :      ||| |||   ::   |||
627 eThrThrLysSerSerProArgGlyGluLeuArgGlyGlnValHisIleA 644

274 .....GCGGCC 279
      :::
644 laSerGlnCysGluAlaGlyGlyLeuArgLeuAlaSerGluGlyValGln 660

280 TGACCCCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGC 329
    +++|||   ::   ::|||:::   ::   ::|||:::|||   ||
661 MetProLeuAlaProAsnGlyGluAlaAlaThrSerProMetLeuProAl 677

330 TGGGACT...CGCGCTGCTCTGGTTCCCCCT.....GGACTCCACGCT 370
    |||      ||| |||||   |||   |||   ::
677 aGlyProGlyProGluAlaProValProAlaLysHisGlySerPro.Gly 693

371 CGAGCCCGCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCC 420
    ||| |||   |||:::||||:::||||:::
694 ArgProArgAspProAsnThrCysPheGluGlyGlnArgProHi 710

421 CGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCCTGATGTACTGCC 470
    ||| ||| |||   ::|||
710 sGlyAlaArgTrpAlaProAsnTyrAspPro.....LeuCyss 723

```

FIG. 2C (CONT.)

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471	TGGCTGTACCTGCTCAGAGCGGCCCATGTGAGTTGTTACCGCCTCCAC	520
	::: :: : :	
723	erLeuCysIleCysGlnArgThr...ValIleCysAspProValVal	738
521	TGTCCGCCTGTCCACTGCCCCCCAGCCTGTGACGGAGCCCACAGCAATGCTG	570
	: :	
739	CysProProSerCysProHisProValGlnAlaLeuAspGlnCysCy	755
571	TCCCAAAGTGTGTGGAA.....CCTCACACTCCCT	599
755	sProValCysProGluLysGlnArgSerArgAspLeuProSerLeuProA	772
600	CTGGACTCCGGGCCACCACCAAGTCCTGCCAGCACAACGGGACCATTGTAC	649
	: : : : : : : : :	
772	sn.....LeuGluProGlyGluGlyCysTyrrPheAspGlyAspArgSer	786
650	CAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCCTCCCGCCTGCC	699
	: : : : : : : :	
787	TrpArgAlaAlaGlyThrArgTrpHisProValValProPropheGlyLe	803
700	CAACCAGTGTCTCTGCAGCTGC.....ACAGAGGGCCAGATCTACT	743
	: : : : : : : : : : : : : : : :	
803	uileLysCysAlaValCysThrCysLysGlyAlaThrGlyGluValHisc	820

FIG. 2C (CONT.²)

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```
744 GCGGCCTCACAACCTGCCCCGAACCAAGGCTGCCAGACACCCCTCCCGCTG 793
      ||      ::  |||||:::  ::|||  ||:::
820 ysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArgAla 836

794 ...CCAGACTCCTGCTGCCAAGCCTGCAAAAGATGAGGCAAGTGAGCAATC 840
      |||  :::|||||:::  |||
837 AsnProThrAspCysCysLysGlnCys..... 845

841 GGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGG 890

845 ..... 845

891 ATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGCC 940
      |||:::

846 .....ProVal 847

941 CCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACC 990
      :::|||  :::|||  ||:::  ||
848 GlySerGlyThrAsnAlaLysLeuGlyAspProMetGlnAlaAspGlyPr 864

991 CAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCCTGAAGGAGAAACATA 1040
      |:::|||

864 oArgGly..... 866
```

FIG. 2C (CONT.)

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1041 NGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGG 1090
||| ::|||::: :: ::::: |||
867CysArgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrp 880

1091 CACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCTG 1140
|||||::: ||||| ||||| ||| ||
881 HisProSerValProPheGlyGluMetSerCysIleThrCysArgCy 897

1141 TGAGGATGGCCCGCAGGACTGCCAGCGTGTGACCTGTCCCACGAAGTACC 1190
| ||| |||::: ||| |||
897 sGlyAlaGlyValProHisCysGluArgAspCysSerProProLeuS 914

1191 CCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGTC... 1237
||| ::::: ::::: |||||::: |||
914 erCysGlySerGlyLysGlu.....SerArgCysCysSerHisCysThr 928

1238CCAGAGGACAAAGCAGACCC 1257
||||| ::: :::
929 AlaGlnArgSerSerGluThrArgThrLeuProGluLeuGluLysGluAl 945

1258 TGGCCACAGT 1267
|||||
945 aGluHisSer 948

FIG. 2C (CONT.)

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656 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCAGTGATGCTGG 705
||| ||| ::::: ||| ::|
3 SerTyrHisArgSerHisTyrAspProProSerArgGlnAlaGlyG1 19
706 GAGAAAGAGAGCGCCCGGCACCCACCCACCCCTGCGCTCAGCGCCCTC 755
| ::||| |||||::: ::|
19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33
756 TGAGCTTCATCCCTCGCCACTTCAGACCCCAAGGAGCAGGAGCACAAC 805
::: ::| :::::|
34MetAspSerGlnGlnAlaSerGlyThrIle 43
806 GTC AAGATCGTCCTG.....AAGGAGAAACATANGAAAGCCTGTGTGCA 849
|:::|::|:::|:::|:::|:::|:::|
44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValse 60
850 TGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCCGGCTTCCCGTG 899
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77

FIG. 3A

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900 CCTTCGGCCCTTGCCCCATGCATCCTATGCACCTGTGAGGATGCCCGCCAG 949
||||| ||||:||||| ||||: ||||
77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

950 GACTGCCAGCGTGTGACCTGTCCCACGAAGTACCCCTGCCGTCAACCCEGA 999
:::||||:||||: |||||:||||: |||||:||||: |||||:
94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGl 110

1000 GAAAGTGGCTGGGAAGTGTGCAAGATTGCCCCAGAGACAAGCAGAC. 1048
:||||: ||||| ||||| |||||:||||| |||||
110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1049CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1087
|||||:|||| :|| :|||: |||| :||
127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1088 GCACCGGCGGGTCTCGTCCACACATCGGTA...TCCCCAAGCCCCAGA 1134
:: ||||: ||||| :||| :||
144 Glu.....ThrMetProValTyrGluSerValPheMetGluAspGlyGl 158

FIG. 3A (CONT.)¹

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```
1135 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCCTCGGACTTGGTGGAGA 1184
      :::: |||:::||||| ||| |||||:
158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175
1185 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1234
      :::::|||| ::
175 alHisValTrpThrIle..... 180

1235 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1284
      |||:::||||| ||
181 .....ArgLysGlyIleLeuGlnHisPheHis.....Il 190

1285 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGACAGCAGCAGCTCCGAC 1334
      |:::||||:: |||:: |||:: |||:::|
190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206

1335 TGCTCGCTGGCCCCCAGGAAGGTCACTGGAACGCTCTTCCTAGCCCCAGACC 1384
      ||:::|::: |:::|:::|:::|:::|
206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222

1385 CTGGAGCTGAAGGTCACGGGCCAGTCCAGACAAAGTGACCAAGACATAACA 1434
      :::::|::: |:::|
223 AlaGlnIleSerGlnMetCysSer..... 230
      +++
```

FIG. 3A (CONT.)

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```
1435 AAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATAT 1484
      ::: ||||| ||||| :::
231 ....SerArgValCysArgThrGluLeuGluAspLeuValLysValLeu 246
      1485 TAATAAATAAGAAAGTTGCATAAACCAT 1510
          ::::::::::: ::|||
246 yrLeuGluArgSerGluLysGlyHis 254
```

FIG. 3A (CONT.³)

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```

368 CCCACTGTGGAACCTCACA CTCCCTCTGGACTCCGGGCCCCCA.....CC 411
    |||::: ||| |||::: ||| ||| |||
532 ProAlaLeuAlaProAlaLysProGlyGlyProGlyArgProArgAspPr 548
    |||::: ||| |||::: ||| ||| |||
412 AAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCA 461
    |::: ||| ::||| ::| ||||| ::|
548 oAsnThrCysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTrpA 565
    |::: ||| ::||| ::| ||||| ::|
462 GTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAG.....TGT 502
    :: ||||| |||
565 la.....ProAsnTyrAspProLeuCys 572
    :: ||||| |||
503 GTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAAACCTG 552
    |||||::: ||| ::| ||| ::: |||
573 SerLeuCysThrCysGlnArgArgThrValIleCysAspProValValCy 589
    |||||::: ||| ::| ||| ::: |||
553 CCCCGAACCAAGCTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGTGCC 602
    |||| |||::: ||||| |||::: |||||::: |||||
589 sProProSerCysProHisProValGlnAlaProAspGlnCysCysP 606
    |||| |||::: ||||| |||::: |||||::: |||||
603 AAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGACAGTGTG 652
    ::||| |||::: |||||
606 roValCys.....ProGluLysGlnAspVal 614
    ::||| |||::: |||||

```

FIG. 3B

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```

653 CAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCA.....TG TTC 693
      :::::| | | | | | | | | | | | | | | | | | | | | |
615 ArgAspLeuProGlyLeuProArgSerArgAspProGlyGluGlyCysTy 631

694 CAGTGATGCTGGGAGAAAG...AGAGGCCCGGGCACC..... 727
      | | | | | | | | | | | | | | | | | | | | | |
631 rPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArgTrpHisProV 648

728 ..CCAGCCCCCACTGGCCTC..... 745
      | | | | | | | | | | | | | | | | | | | | | |
648 a1ValProProPheGlyLeuIleLysCysAlaValCysThrCysLysGly 664

745 ..... 745

665 GlyThrGlyGluValHisCysGluLysValGlnCysProArgLeuAlaCy 681

746 .AGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTC.....AGACCCA 785
      ::: | | | | | | | | | | | | | | | | | | | | |
681 sAlaGlnProValArgValAsnProThrAspCysCysLysGlnCysProV 698

```

FIG. 3B (CONT.)

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```

786 AGGAGCAGGCAGC...ACAACTGTCAAGATCGTCCTGAAGGAGAGAAACAT 832
      |||:::||||:::      :::      :::::
698 aIGlySerGlyAlaHisProGlnLeuGlyAspProMetGlnAlaAspGly 714
      :::::||||      :::||||:::      :::      :::::||||
833 ANGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTG 882
      :::::||||      :::||||:::      :::      :::::||||
715 ProArgGlyCysArgPheAlaGlyGlnTrpPheProGluSerGlnSerTr 731
883 GCACCCGGCCCTTCCCGTGCCTTCGGCCCTTGCCCATGCATCCTATGCACCT 932
      |||||||:::      ||||||      |||||      |||      |
731 pHisProSerValProProPheGlyGluMetSerCysIleThrCysArgC 748
933 GTGAGGATGGCCCGCCAGGACTGCCAGCGGTGTGACCTGTCCCACGAAGTAC 982
      ||      |||      |||:::||||      |||
748 ysGlyAlaGlyValProHisCysGluArgAspAspCysSerLeuProLeu 764
983 CCCTGCCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGC... 1030
      |||      :::::      :::::|||||:::      |||
765 SerCysGlySerGlyLysGlu.....SerArgCysCysSerArgCysTh 779
1031 .....CCAGAGGACAAAGCAGACCCCT 1051
      |||||      :::::|||||
779 rAlaHisArgArgProAlaProGluThrArgThrAspPro 792

```

FIG. 3B (CONT.²)

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1031 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCAGTGATGCTGG 1080
||| ||| ::::: ||| ::| ::||
3 SerTyrHisArgSerHisTyrAspProProSerArgGlnAlaGlyG1 19
1081 GAGAAAGAGAGGCCCCGGGCACCCCCCAGCCCCCTCAGCCCTCAGCGCCCCCTC 1130
| ::||| |||||::: ::| |||
19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33
1131 TGAGCTTCATCCCTCGCCACTTCAGACCCCAAGGGAGCAGGCAGCACAACT 1180
::: ::| ||:::|::|
34MetAspSerGlnGlnAlaSerGlyThrIle 43
1181 GTCAAGATCGTCCTG.....AAGGAGAAACATANGAAAGCCTGTGTGCA 1224
||:::|||||::: ||:::||||| :::::|||||
44 valGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValSe 60
1225 TGGCGGGAAGACGTACTCCCCACGGGGAGGTGTGGCACCCCGGCCCTCCCGTG 1274
:::||||| ||||| ||||| ||||| ||||| :::|||||
60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77

FIG. 4A

FIG. 4A (CONT.)¹⁾

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```
1510 CAACCTGCGTCGCTTGCCCTGGAAACACGAGGCTCGGACTTGGTGGAGA 1559
      :::: |||:::||||||| ||| |||||:
158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1560 TCTACCTCTGGAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNN 1609
      :::::||||| :::
175 alHisValTrpThrIle..... 180

1610 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1659
      |||:::||||||| ||
181 .....ArgLysGlyIleLeuGlnHisPheHis.....Il 190

1660 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGAC 1709
      |:::||||::: |||::: |||::: ||| |||||:::|
190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206

1710 TGCTCGCTGCCCCCAGGAGTCAGTGAACGTCTTCCTAGCCAGACC 1759
      ||:::|:::|
206 euValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGlu 222
```

FIG. 4A (CONT.)

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```

792 CCTGCCAGCACAAACGGGACCATGTACCAACACGAGAGATCTTCAGTGCC 841
   ::|||   ::|||   ::   ::|||::   ::
768 lYCysTyrPheGluGlyAspGlnLysMetHisAlaProGlyThrThrTrp 784

842 CATGAGCTGTTCCCTCCCGCCTGCCCAACCAAGTGTCTCTGCAGCTG 891
   |||   ::   |||   ::|||:::~::~|||::~::~|||
785 HisProPheValProProPheGlyTyrIleLysCysAlaValCysThrCy 801

892 C.....ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGAAC 935
   |   ::   |||:::~::~|||   ::|||~::~|||
801 sLysGlySerThrGlyGluValHisCysGluLysValThrCysProProL 818

936 CAGGCTGCCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAAGCC 982
   |||   |||::~::~|||:::~::~|||~::~|||~::~|||
818 euThrCysSerArgProIleArgArgAsnProSerAspCysCysLysGlu 834

983 TGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTC 1032
   |||   |||   ::   :::~::~|||~::~|||   ::|||~::~|||
835 CysProProGluGluThrProProLeuGluAspGluGluMetMetGlnAl 851

```

FIG. 4B (CONT.¹)

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```
1033 GCTCCATGGGTGAGACATCCTCAGGATCCATGTTCAGTGATGCTGGGA 1082
      :
851 a..... 851

1083 GAAAGAGAGGCCCGGCACCCAGCCCCCACTGGCCTCAGCGCCCTCTG 1132
      |||||
852 .....AspGlyThr..... 854

1133 AGCTTCATCCCTCGCCACTTCAGACCCCAAGGAGCAGGCACAACTGT 1182
      :
854 ..... 854

1183 CAAGATCGTCCTGAAGGAGAAACATANGAAAGCCTGTGTGCATGGCGGA 1232
      :: ||| ||| :
855 .....ArgLeuCysLysPheGlyLysA 862

1233 AGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCCTTCGGC 1282
      :: |||:::|||| |||||::: |||
862 snTyrTyrGlnAsnSerGluHisTrpHisProSerValProLeuValGly 878
```

FIG. 4B (CONT.)

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1283 CCTTGCCCATGCATCCTATGCACCTGTGAGGATGGCCGCGAGGACTGCCA 1332
||||| ||| |||::: ||| |||||
879 GluMetLysCysIleThrCysTrpCysAspHisGlyValThrLysCysG1 895

1333 GCGTGTGACCTGTCCCACGAAAGTACCCCTGCCCGTCACCCCGAGAAAGTGG 1382
|||| | ||||| |||||::: ||| :::::
895 nArgLysGlnCysProLeu...LeuSerCysArgAsnProIleArgThrG 911

1383 CTGGGAAGTGCTGCAAGATTGCCCCAGAGGAC 1414
||||| ||||| ||||| |||||
911 luGlyLysCysCysProGluCysIleGluAsp

FIG. 4B (CONT.³)

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560 TGCCTTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTA 609
||| |||:::||||::: ::| ||::: ||| |||
693 CysSerPheGluGlyGlnLeuArgAlaHisGlySerArgTrpAlaProAs 709

610 CTTGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 659
::: ::| ||| |||:::||||:::|
709 pTyrAspArgLys.....CysSerValCysSerCysGlnLysA 722

660 GCGCCCATGTGAGTTGTACCGCCTCCACTGTCCGCCTGTCCACTGCCCC 709
::: ||| ||| ::| ||| ||| |||:::|
722 rgThr...ValIleCysAspProIleValCysProProLeuAsnCysSer 737

710 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCA 759
||||| |||:::||||| ||| |||
738 GlnProValHisLeuProAspGlnCysCysProValCysGluGluLysLy 754

760 CACTCCCTCTGGACTCCGGGGCCCCACCAAGTCCTGCCAGCACACGGGA 809
:::| ||| :::| ::|
754 sGluMetArgGluValLysLysProGluArgAlaArgThrSerGluGlyC 771

FIG. 4C

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```

810 CCATGTACCAACACGGAGAGATCTTCAGTGCC.....CAT 844
      ::::: ::::: ::::: ::::: |||
771 ysPhePheAspGlyAspArgSerTrpLysAlaAlaGlyThrArgTrpHis 787
      :: ||| ::::: ::::: ::::: ::::: |||
845 GAGCTGTTCCCCCTCCCGCCTGCCCAACCCAGTGTCTCTGCAGCTGC.. 892
      :: ||| ::::: ::::: ::::: ::::: |||
788 ProPheValProProPheGlyLeuIleLysCysAlaIleCysThrCysLy 804
      :::: ACAGAGGGCCAGATCTACTGCGGCTCACAACTGCCCCGAACCAG 938
      :::: ||::: ::::: ||| ::::: ||| ::::: :
804 sGlySerThrGlyGluValHisCysGluLysValThrCysProLysLeuS 821
      :::: ||::: ||::: ||::: ||::: ||::: ||::: |||
939 GCTGCCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAAGCCTGC 985
      ::||| ||::: ||::: ::::: ::::: ||| ::::: |||
821 erCysThrAsnProIleArgAlaAsnProSerAspCysCysLysGlnCys 837
      :::: AAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCT 1035
      ||| :::: ::::: ||::: ||::: ||::: ||::: |||
838 ProValGluGluArgSerProMetGluLeuAlaAspSerMetGlnSer.. 853

```

FIG. 4C (CONT.)¹⁾

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1036 CCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAA 1085
853 853
1086 AGAGAGGCCCCGGGCACCCAGCCCCCACTGGCCTCAGCGCCCTCTGAGC 1135
853 853
1136 TTCATCCCTCGCCCACTTCAGACCCCAAGGAGCAGGCAGCACAACTGTCAA 1185
|||||
854AspGlyAlaGlySer..... 858
1186 GATCGTCCTGAAGGAGAAACATANGAAAGCCTGTGTGCATGGCGGGAAGA 1235
||| |||
859CysArgPheGlyArgHisT 865
1236 CGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCT 1285
||| ::: ||| |||||::: |||||
865 rpTyrProAsnHisGluArgTrpHisProThrValProPheGlyGlu 881
1286 TGCCCATGCATCCTATGCACCTGTGAGGATGGC.....CG 1320
|||::: |||||::: |||
882 MetLysCysValThrCysThrCysAlaGluGlyIleThrGlnCysArgAr 898

FIG. 4C (CONT.²)

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```
1321 CCAGGACTGCCAGCGTGTGACCTGTCCACGAAAGTACCCCTGCCGTCACC 1370
      ||||:::||||      :::|||||  |||
898 gGlnGluCysThrGlyThrThrCysGlyThr..... 908

1371 CCGAGAAAGTGGGAGTGCTGCAAGATTGCCCCAGAGGACAAAGCA 1420
      :::      :::|||||  |||  :::  :::
909 ..GlySerLysArgAspArgCysCysThrLysCysLysAspAlaAsnGln 924

      1421 GACCCCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCC 1459
      |||  :::::  :::  :::::|||||  |||
925 AspGluAspGluLysValLysSerAspGluThrArgThrPro 938
```

FIG. 4C (CONT.³)

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536 GGTTGCCAGGCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 585
||| ||| |||:||||:||||:||||:
543 GlyArgProArgAspProAsnThrCysPheGluGlyGlnGlnArgPr 559
586 CCCCCGGGAGAGCTGGCACCCCTACTTGGAGCCACAAAGGCCTGATGTACT 635
||| ||| ||| |||:||||
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.....LeuC 572
636 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 685
|| |||||:||||: ||| ||| |||: |||
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587
686 CACTGTCCGCTGTCCACTGCCCCCGCCCTGTGACGGAGCCACAGCAATG 735
||||| |||||:||||| |||:|||||
588 valCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604
736 CTGTCCCAAGTGTGGAA.....CCTCACACTC 764
||||| ||| ||| |||
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621

FIG. 4D

37/116

```

765 CCTCTGGACTCCGGGCCCCACCAAGTCCTGCCAGCACAAACGGGACCATG 814
    ||   :::   |||   |||   :::::||||   :::|||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

815 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTCCCTCCCGCCT 864
    ::::::   |||   :::   |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProPheG1 653

865 GCCCCAACCAAGTGTCTCTGCAGCTGCACA.....GAGGCCAGATCT 908
    :::|||:::||||:::||||   |||:::~::~:
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

909 ACTGCGGCTCACAACCTGCCCCCGAACCAAGGCTGCCAGCACCCCTCCCG 958
    ::|||   :::   |||||:::   :::|||   |||:::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

959 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAGATGAGGCAAGTGAGCA 1005
    :::   |||   :::|||||~|:::   |||
687 ValAsnProThrAspCysCysLysGlnCys..... 696

```

FIG. 4D (CONT.)

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FIG. 4D (CONT.)

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1300 ATGCACCTGTGAGGATGGCCCGCCAGGACTGCCAGCGTGTGACCTGTCCCA 1349
||| ||| ||| |||::||| |||
745 rCysArgCysGlyAlaGlyValProHisCysGluArgAspCysSerL 762
1350 CGAAGTACCCCTGCCGTCAACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAG 1399
||| ::::: :::::|||||:::
762 euProLeuSerCysGlySerGlyLysGlu.....SerArgCysCysSer 776
1400 ATTTGC.....CCAGAGGACAAAGCAGACCCCT 1426
||| ||||| :::::|||||
777 ArgCysThrAlaHisArgArgProAlaProGluThrArgThrAspPro 792

FIG. 4D (CONT.³)

chordin_ed7	SPLPSAGPSF	VPSLPPFPA	FSFHLSSLPT	LDLPSCPPFL	PTAASWPFSD	
chordin_ed6TR_2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
chordin_ed6TR_1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	51				100	
chordin_ed7	PALAADLLGS	CGLICGPCXS	VSFSSPVLPT	PLPDQRDPG	ERMVPEVRVL	
chordin_ed6TR_2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
chordin_ed6TR_1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	101				150	
chordin_ed7	SSLLGLALLW	FPLDSHARAR	PDMFCLFHGK	RYSPGESWHP	YLEPQGLMYC	40/116
chordin_ed6TR_2	DRVFGLEPPG	TNMALVGLPG	PDMFCLFHGK	RYSPGESWHP	YLEPQGLMYC	
chordin_ed6TR_1	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	151				200	
chordin_ed7	LRCTCSEGAH	VSCYRLHCPP	VHCPQPVTE.	PQCCCPK.CV	EPHTPSGLRA	
chordin_ed6TR_2	LRCTCSEGAH	VSCYRLHCPP	VHCPQPVTE.	PQCCCPK.CV	EPHTPSGLRA	
chordin_ed6TR_1	~~~ISSWGQM	QNHOKSGLVN	FSKDSHETSF	SSSSCPSPTV	EPHTPSGLRA	

FIG. 5

chordin_ed7	201	PPKSCQHNGT	MYQHGEIFSA	HELFP SRLPN	QCVLCSCTEG	QIYCGLTTCP	250
chordin_ed6TR_2		PPKSCQHNGT	MYQHGEIFSA	HELFP SRLPN	QCVLCSCTEG	QIYCGLTTCP	
chordin_ed6TR_1		PPKSCQHNGT	MYQHGEIFSA	HELFP SRLPN	QCVLCSCTEG	QIYCGLTTCP	
chordin_ed7	251	EPGCPAPLPL	PDSCCQACKD	EASEQSD EED	SVQSLHGVRH	PQDPCSSDAG	300
chordin_ed6TR_2		EPGCPAPLPL	PDSCCQACKD	EASEQSD EED	SVQSLHGVRH	PQDPCSSDAG	
chordin_ed6TR_1		EPGCPAPLPL	PDSCCQACKD	EASEQSD EED	SVQSLHGVRH	PQDPCSSDAG	
chordin_ed7	301	RKRGPGTPAP	TGLSAPLSFI	PRHFRPKGAG	STTVKIVLKE	KHXKACVHGG	41/116 350
chordin_ed6TR_2		RKRGPGTPAP	TGLSAPLSFI	PRHFRPKGAG	STTVKIVLKE	KHXKACVHGG	
chordin_ed6TR_1		RKRGPGTPAP	TGLSAPLSFI	PRHFRPKGAG	STTVKIVLKE	KHXKACVHGG	
chordin_ed7	351	KTYSHGEVWH	PAFRAFGPCP	CILCTCEDGR	QDCQRVTCPT	KYPCRHPPEKV	400
chordin_ed6TR_2		KTYSHGEVWH	PAFRAFGPCP	CILCTCEDGR	QDCQRVTCPT	KYPCRHPPEKV	
chordin_ed6TR_1		KTYSHGEVWH	PAFRAFGPCP	CILCTCEDGR	QDCQRVTCPT	KYPCRHPPEKV	

FIG. 5 (CONT.)

401
chordin_ed7 450
AGKCKKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL
chordin_ed6TR_2 AGKCKKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL
chordin_ed6TR_1 AGKCKKICPE DKADPGHSEI SSTRCPKAPG RVLVHTSVSP SPDNLRRFAL

451
chordin_ed7 500
EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD
chordin_ed6TR_2 EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD
chordin_ed6TR_1 EHEASDLVEI YLWKLVKDEE TEAQRGEVPG PRPHSQNFHL TQIKKVRKQD

501
chordin_ed7 542
FQKEAQHFRL LAGPHEGHWN VFLAQTLLELK VTASPDKVTK T*
chordin_ed6TR_2 FQKEAQHFRL LAGPHEGHWN VFLAQTLLELK VTASPDKVTK T*
chordin_ed6TR_1 FQKEAQHFRL LAGPHEGHWN VFLAQTLLELK VTASPDKVTK T*

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FIG. 5 (CONT.)

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```

1106 CCTTCGGCCCTTGCCCTGCATCCCTATGCACCTGTGAGGATGGCCGCCAG 1155
||||||| ::: |||:::|||||||::: |||:::
77 laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

1156 GACTGCCAGCGGTGACCTGTCCCAACCGAGTACCCCTGCCGTACCCCGA 1205
:::||||:::~::~: |||:::~::~: |||:::~::~: |||:::~::~:
94 GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGln 110

1206 GAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGGACAAAGCAGAC. 1254
:||||::: |||~::~: |||~::~: |||~::~: |||~::~: |||~::~:
110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1255 .....CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1293
||||||~::~: ||| ~::~: ||| ~::~:
127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1294 GCACCGGGCGGGTCCCTCGTCCACACATCGGTA...TCCCCAAGCCCGA 1340
::: |||~::~: |||~::~: ~::~: ~::~: ~::~: ~::~:
144 Glu.....ThrMetProValTyrGluSerValPheMetGluAspGlyGln 158

```

FIG. 6 (CONT.¹)

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```
1341 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACCTGGTGGAGA 1390
      :::: ||:::||||| ||| |||||
158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1391 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440
      :::::|||| :::
175 alHisValTrpThrIle..... 180

1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1490
      ||::: |||||
181 .....ArgLysGlyIleLeuGlnHis.PheHis.....I 190

1491 TCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGA 1540
      ||:::||||:: ||::: ||| |||||:::
190 leGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLys 205

1541 CTGCTCGCTGGCCCCCAGCAAGGTCACTGGAACGTCTTCCCTAGCCCAGAC 1590
      ||:::::: :::::||||::::::|||
206 LeuValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyGl 222
```

FIG. 6 (CONT.²)

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```

3  CTCCCCCTTCTTTGATCGCCTCTCC.....CTTCTGCTGGA 40
   |||||  ::::  |||  ||||
390 LeuProProValLysSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 406
   |||||  ::::  |||  ||||

41  CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT..... 71
   |  ||||  ::::  |||
406 pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 423
   |||||  ::::  |||||  +++|||

72  ..TCCCCGCGTTCTTTCCACCTTTTCTCTTCTTCCCCACCTTAGACCTCC 119
   ::  ::::  ::::  ||||  +++|||
423 erGluGlnGlyThrValThrAlaHisLeuLeuGlyProProGlyThr... 438

120 CTTCCTGCCCTCCTTTCCCTGCCCCACCGCTGCTTCCTGGCCCTTCTCCGAC 169
   ||||  ::::  |||

439 .....ProGlyProAr 442

170 CCGCTCTAGCAG.....CAGACCTCCTGGGGTCTGTGGGTG 207
   |||++::  ::  ::  ||::  |
442 gArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyValValLysA 459

```

FIG. 7

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```
208 ATCTGTGGCCCTGTGCCTCCGTGTCCCTTTTCGTCTCCCTTCCCTCCCGAC 257
      ||||| ||| ||||| |||
459 spLeuGluProGluLeuLeuArgHisLeu..... 468

258 TCCGCTCCCGACGAGCGCCTGACCTGGGAAAGGATGGTTCC...CG 304
      ||| ||| |||:::++| ||||| ||
469 ...AlaLysGlyMetAlaSerLeuLeuIleThrLysGlySerProAr 484

305 AGGTGAG.....GGTC 315
      ||||| |||
484 gGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyG 501

316 CTCTCCTCCTT.....GCTGGGACTCGCGCT..... 341
      ||| ||| |||:::|||||
501 lyLeuArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAla 517

342 .....GCTCT 346
      |||||
518 ProAspProAlaSerAlaAlaProProValProGlyLeuProAlaLe 534
```

FIG. 7 (CONT.¹)

FIG. 7 (CONT.²)

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586CCTCACACTCCCTCTGGACTCCGGGCCCCACCAA 619
||| ||| ::: ||| ||| :
612 nAspValArgAspLeuProGlyLeuProArgSer...ArgAspProGlyG 628

620 AGTCCTGCCAGCACAAACGGGACCATGTACCAACACGAGAGATCTTCAGT 669
::: ||| ||| :
628 luGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArg 644
::: ||| ||| :
670 GCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAG 719
||| ::| ||| :
645 TrpHisProValValProPheGlyLeuIleLysCysAlaValCysTh 661
::: ||| :
720 CTGCACA.....GAGGGCCAGATCTACTGCGGGCTCACAACTGCCCCG 763
: ||| ||| :
661 rCysLysGlyGlyThrGlyGluValHisCysGluLysValGlnCysProA 678

764 AACCAGGCTGCCCCAGCACCCCTCCCGCTG...CCAGACTCCTGTGCCAG 810
:: : ||| ||| :
678 rgLeuAlaCysAlaGlnProValArgValAsnProThrAspCysCysLys 694

FIG. 7 (CONT.³)

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811 GCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACCGTGTGCA 860
|||
695 GlnCys..... 696

861 GTCGCTCCATGGGTGAGACATCCTCAG.....GATCCATGTTCCAGTG 904
::: :::: ||||| ||||| :::::|
697 .ProValGlySerGlyAlaHisProGlnLeuGlyAspProMetGlnAlaA 713

905 ATGCTGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCCCTGCGCCTCAGC 954
|| |||||
713 sp.....GlyPro..... 715

955 GCCCCCTCTGAGCTTCATCCCTCGCCCACTTCATACCCAAGGAGCAGGCAG 1004

715 715

1005 CACAACGTGTCAAGATCGTCCCTGAAGGAGAAACATAAGAAAGCCTGTGTGC 1054
::: ::::|
716ArgGlyCysArgP 720

FIG. 7 (CONT.⁴)

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```

1055 ATGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCCTTCCGT 1104
      ::|||:::   ::   :::::   ::||||||:::
720 heAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerValPro 736

1105 GCCTTCGGCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCA 1154
      |||||   ::   |||||   |||   |||   |||
737 ProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyValPr 753

1155 GGAAGTCCAGCGTGTACCTGTCCACCGAGTACCCCTGCCGTACCCCG 1204
      |||:::|   |||   |||   :
753 oHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySerGlyL 770

1205 AGAAAGTGGCTGGGAAGTGTGCAAGATTGCAAGATTTGC..... 1236
      :::::   :::::   |||:::   |||
770 ysGlu.....SerArgCysCysSerArgCysThrAlaHisArgArgPro 784

1237 ...CCAGAGGACAAAGCAGACCCT 1257
      |||||   :::::~|||||
785 AlaProGluThrArgThrAspPro 792

```

FIG. 7 (CONT.⁵)

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```
3  CTTCCCCCTTTCTTTGATCGCCTCTCC.....CTTCTGCTGGA 40
   ||||||| : : : : : ||| |||||
540 LeuProProValArgSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 556

41 CCTTCCTTCGTCCTCCATCTCTCCCTCCTT.....T 72
   | ||||| : : : : : |
556 pThrHisCysHisLeuHisTyrGluValLeuAlaGlyLeuGlyGlyS 573

73 CCCCCGTTCTCTTCCACCTTTCTCTTCTTCTCCACCTTAGACCTCCCTT 122
   || : : : : : |||
573 erGluGlnGlyThrValThr..... 579
      ++

123 CCTGCCCCCTTCTCTGCCACCGCTGCTTCTCTGGCCCTTCTCCGACCCC 172
   ||| ||| ||||| : : |||||||
580 ...AlaHisLeuLeuGlyProProGlyMetProGlyPro..... 591

173 GCTCTAGCAGCAG.....ACCTCCTGGGGTC 198
   +++||| : : : |||
592 .....GlnArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyV 606
```

FIG. 8

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```
199 TGTGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTT 248
    ::      |||||      |||:::      |||||      |||
606 alVallYsAspLeuGluProValLeuLeuArgHisLeu..... 618

249 CCTCCCGACTCCGCTCCCGGACCAGCGGCC..... 278
    |||      |||      |||:::
619 .....AlaGlnGlyThrAlaSerLeuLeuIleThrThrLysSe 631

278 ..... 278

631 rSerProArgGlyGluLeuArgGlyGlnValHisIleAlaSerGlnCysG 648

279 .....TGACCCCTGGGA 290
    +++|||      :::
648 luAlaGlyGlyLeuArgLeuAlaSerGluGlyValGlnMetProLeuAla 664

291 AAGGATGTTCCCGAGGTGAGGTCCTCTCCTCCTTGCTGGGACT...CG 337
    ::|||:::      :::      ::|||:::|||      |||||
665 ProAsnGlyGluAlaAlaThrSerProMetLeuProAlaGlyProGlyPr 681
```

FIG. 8 (CONT.¹)

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```

338 CGCTGCTCTGGTCCCCCT.....GGACTCCACGCTCGAGCCCGCCCA 381
    ||| ||||| ||| ||| ::||| |||
681 oGluAlaProValProAlaLysHisGlySerPro.GlyArgProArgAsp 697
    ||| ||||| ||| ||| ::||| |||

382 GACATGTTCTGCCCTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTG 431
    |||:::||||:::||||::: ||| |||
698 ProAsnThrCysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTr 714
    ||| ||| ::||| ||| ||| |||

432 GCACCCCTACTTGGAGCCACAAAGGCCTGATGTACTGCCCTGCCGTGTACCT 481
    | ||| ::||| ||| ||| |||
714 pAlaProAsnTyrAspPro.....LeuCysSerLeuCysIleC 727

482 GCTCAGAGGGGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTC 531
    ||::: :: ||| ||| :: |||||
727 ysGlnArgArgThr...ValIleCysAspProValValCysProProPro 742

532 CACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGT 581
    |||||:::||||| ::||| ||||| |||
743 SerCysProHisProValGlnAlaLeuAlaAspGlnCysCysProValCysPr 759

```

FIG. 8 (CONT.²)

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582 GGAA.....CCTCACACTCCCTCTGGACTCCGGG 610
||| ||| |||:
759 oGluLysGlnArgSerArgAspLeuProSerLeuProAsn.....LeuG 774
611 CCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAG 660
||| ::::: ||| ::::: |||
774 luProGlyGluGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAla 790
661 ATCTTCAGTGCCCATGAGCTGTTCCTCCCTCCCGCTGCCCAACCAGTGTGT 710
||| ::::: ||| ::::: |||:
791 GlyThrArgTrpHisProValValProProPheGlyLeuIleLysCysAl 807
711 CCTCTGCAGCTGC.....ACAGAGGCCAGATCTACTGCGGGCTCACAA 754
::: |||::: ||| ::::: |||:
807 aValCysThrCysLysGlyAlaThrGlyGluValHisCysGluLysValG 824
755 CCTGCCCCGAACAGGCTGCCCAGCACCCCTCCCGCTG...CCAGACTCC 801
||| |||::: ::::: |||:
824 lnCysProArgLeuAlaCysAlaGlnProValArgAlaAsnProThrAsp 840

FIG. 8 (CONT.³)

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```

802 TGCTGCCAGGCTGCAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGA 851
      |||||::: ||
841 CysCysLysGlnCys..... 845
852 CCGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCA 901
      ||| :::|
846 .....ProValGlyS 849
902 GTGATGCTGGGAGAAAGAGAGGCCCGGCGACCCAGCCCCCACTGGCCTC 951
      || ::::: ||| |||
849 erGlyThrAsnAlaLysLeuGlyAsp.....ProMetGlnAla 861
952 AGCGCCCTCTGAGCTTCATCCCTCGCCACTTCATACCCAAGGGAGCAGG 1001
      :::::|
862 AspGlyPro..... 864
1002 CAGCACAACTGTCAAGATCGTCCCTGAAGGAGAAACATAAGAAAGCCTGTG 1051
      :::::|
865 .....ArgGlyCysA 868

```

FIG. 8 (CONT.⁴)

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```

1052 TGCATGGCGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCCCTTC 1101
      ::|||:::   :::   :::   :::   |||||:::
868  rgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrpHisProSerVal 884

1102 CGTGCCTTCGGCCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCG 1151
      |||||   :::   |||||   |||   |||   |||
885  ProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 901

1152 CCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCCGTCACC 1201
      |||:::| | |   |||   |||
901  lProHisCysGluArgAspCysSerProProLeuSerCysGlySerG 918

1202 CCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGC..... 1236
      :::::   :::::| | | | |:::   |||
918  lYlysGlu.....SerArgCysCysSerHisCysThrAlaGlnArgSer 932

1237 .....CCAGAGGACAAAGCAGACCCCTGGCCACAGT 1266
      |||||   :::   :::   |||||
933  SerGluThrArgThrLeuProGluLeuGluLysGluAlaGluHisSer 948

```

FIG. 8 (CONT.⁵)

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862 TCGCTCCATGGGGTGAGACATCCCTCAGGATCCATGTTCCAGTGATGCTGG 911
||| ||| ::::: ||| ::|
3 SerTyrHisArgSerHisTyrAspProProSerArgGlnAlaGlyG1 19

912 GAGAAAGAGAGGCCCCGGGCACCCCCAGCCCCCTGCGCCTCAGCGCCCTC 961
| ::||| |||||::: ::|
19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

962 TGAGCTTCATCCCCTCGCCACTTCAGACCCCAAGGAGCAGCAGCACAAC 1011
::: ::| |||:::|
34MetAspSerGlnGlnAlaSerGlyThrIle 43

1012 GTCAAGATCGTCCTGAAGGAGAAACATAAG.....AAAGCCTGTGTGCA 1055
||:::|||||:::| ||||| :::|
44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValse 60

1056 TGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCCGCCTCCGTG 1105
:::||||| ||||| ||||| ||||| ::|
60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77

FIG. 9

FIG. 9 (CONT.)

1341 CAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1390
 ::: |||:::||||| ||| |||||:
158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1391 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNN 1440
 :::||||| :::
175 alHisValTrpThrIle..... 180

1441 NNN 1490
 |||::: ||||| |
181ArgLysGlyIleLeuGlnHis.PheHis.....I 190

1491 TCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGA 1540
 ||:||||::: |||::: ||| ||| |||:::
190 leGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLys 205

1541 CTGCTCGCTGGCCCCCACCAGGTCACCTGGAACGTCTTCCTAGCCCAGAC 1590
 |||:::|::: |||:::|:::|:::|:::|:::
206 LeuValThrArgThrThrLeuSerGlnTrpLysIlePheThrGluGlyG1 222

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FIG. 9 (CONT.²)

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```
1591 CCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAAC 1640
      :::::::::::      ::|||
      +++
222 uAlaGlnIleSerGlnMetCysSer..... 230

1641 AAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATA 1690
      ::: ||||| ||||| :::
      SerArgValCysArgThrGluLeuGluAspLeuValLysValLeu 245

1691 TTAATAAATAAGAAGTTGCATAACCAT 1717
      :::::::::::      ::|||
      TyrLeuGluArgSerGluLysGlyHis 254
```

FIG. 9 (CONT.³)

63/116

```

3  CTTCCCCCTTCTTTGATGCGCTCTCC.....CTTCTGTGGA 40
   |||||  ::::  |||  ||||
390  LeuProProValLysSerGlnAlaAlaGlyHisAlaTrpLeuSerLeuAs 406
   41  CCTTCCTTCGTCTCTCCATCTCTCCCTCCTT..... 71
      |  |||||  :::::|||
406  pThrHisCysHisLeuHisTyrGluValLeuLeuAlaGlyLeuGlyGlyS 423
   72  ..TCCCCGGTTCTCTTTCCACCTTCTCTTCTTCTCCACCTTAGACCTCC 119
      ::  :::::  ||::  |||||++|||
423  erGluGlnGlyThrValThrAlaHisLeuLeuGlyProProGlyThr... 438
   120  CTTCCCTGCCCTCCTTTCCTGCCCCACCGCTGCTTCTCTGGCCCTTCTCCGAC 169
      |||:::|
439  .....ProGlyProAr 442
   170  CCCGCTCTAGCAG.....CAGACCTCCTGGGGTCTGTGGGTG 207
      |||++::  ::  ::  ||::  |
442  gArgLeuLeuLysGlyPheTyrGlySerGluAlaGlnGlyValValLysA 459
```

FIG. 10

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208 ATCTGTGGCCCTGTGCCTCCGTGTCCCTTTTCGTCTCCCTTCCCTCCCGAC 257
||||| ||| ||||||| |||
459 spLeuGluProGluLeuLeuArgHisLeu..... 468
258 TCCGCTCCCGACGACGCGCCTGACCCCTGGGGAAGGATGGTTCC...CG 304
||| ||| |||:::++
469 ...AlaLysGlyMetAlaSerLeuLeuIleThrThrLysGlySerProAr 484
305 AGGTGAG.....GGTC 315
|||||||
484 gGlyGluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyG 501
316 CTCTCCTCCTT.....GCTGGGACTCGCGCT..... 341
||| ||| |||:::|||||
501 lLeuArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAla 517
342GCTCT 346
|||||
518 ProAspProAlaSerAlaAlaProProValValProGlyLeuProAlaLe 534

FIG. 10 (CONT.¹)

65/116

347 GGTCCC.....CCTGGACTCCACGCTCGAGCCCGCCAGACATGTTC 390
|:::| | | | | | | | | | | | | | | | | | | | | |
534 uAlaProAlaLysProGlyGlyPro.GlyArgProArgAspProAsnThr 550
391 TGCCTTTCCATGGGAAGAGATACTCCCCCGCGGAGAGCTGGCACCCCTA 440
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
551 CysPhePheGluGlyGlnGlnArgProHisGlyAlaArgTrpAlaProAs 567
441 CTTGGAGCCACAAGGCTGATGTACTGCCCTGGCTGTACCTGCTCAGAGG 490
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
567 nTyrAspPro.....LeuCysSerLeuCysThrCysGlnArgA 580
491 GCGCCCATGTGAGTTGTACCGCCTCCACTGTCCGCCCTGTCCACTGCCCC 540
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
580 rgThr...ValIleCysAspProValValCysProProProSerCysPro 595
541 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAGTGTGTGGAA..... 585
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
596 HisProValGlnAlaProAspGlnCysCysProValCysProGluLysGl 612

FIG. 10 (CONT.²)

66/116

```
586 .....CCTCACA...CCTCAGTCCCTCTGGACTCCGGGCCCCACCAA 619
    ||| ||| :: ||| ||| :
612 nAspValArgAspLeuProGlyLeuProArgSer...ArgAspProGlyG 628

620 AGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGT 669
    ::::||| ::||| :::::
628 luGlyCysTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArg 644

670 GCCCATGAGCTGTTCCCTCCCGCTGCCCAACCCAGTGTGTCTCTGCAG 719
    ||| :: ||| ::::|||:::||||:
645 TrpHisProValValProPheGlyLeuIleLysCysAlaValCysTh 661

720 CTGCACA.....GAGGGCCAGATCTACTGCGGGCCTCACAAACCTGCCCG 763
    :||| |||:::~::~:~:: ~:: |||||:
661 rCysLysGlyGlyThrGlyGluValHisCysGluLysValGlnCysProA 678

764 AACCAGGCTGCCAGCACCCCTCCCGCTG...CCAGACTCCTGCTGCCAG 810
    :: ::::||| |||::: ~:: ||| ~::|||~::~:
678 rgLeuAlaCysAlaGlnProValArgValAsnProThrAspCysCysLys 694
```

FIG. 10 (CONT.³)

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```
811 GCCTGCAA...GGTGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGT 857
      |||      |||:::~::~:
695 GlnCysProValGlySerGlyAla..... 702

858 GCAGTCGCTCCATGGGTGAGACATCCTCAG.....GATCCATGTTCCA 901
      |||||      |||||  :::
703 .....HisProGlnLeuGlyAspProMetGlnA 712

902 GTGATGCTGGGAGAAAGAGAGGCCCGGCACCCAGCCCCCCTGCGCCTC 951
      ::|||      |||||
712 laAsp.....GlyPro..... 715

952 AGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGAGCAGG 1001
715 ..... 715

1002 CAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTG 1051
      :::~::~:
716 .....ArgGlyCysA 719
```

FIG. 10 (CONT.⁴)

1052 TGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTC 1101
 :::||||::: ::: ::: ::: ::: ::: ::: ::: ::: :::
719 rgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerVal 735

1102 CGTGCCTTCGGGCCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCG 1151
 ||||| ::: ||||| ||| ||| ||| ||| ||| |||
736 ProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 752

1152 CCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCCGTCACC 1201
 ||||:::|||| ||| ||| ||| ||| ||| ||| |||
752 lProHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySerG 769

1202 CCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGC..... 1236
 ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
769 lyLysGlu.....SerArgCysCysSerArgCysThrAlaHisArgArg 783

1237CCAGAGGACAAAGCAGACCCCT 1257
 ||||| ::: ::: ::: ::: ::: ::: ::: ::: :::
784 ProAlaProGluThrArgThrAspPro 792

FIG. 10 (CONT.⁵)

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655 TCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGG 704
||| ||| ::::: ||| ::|
3 SerTyrHisArgSerHisTyrAspProProSerArgGlnAlaGlyG1 19

705 GAGAAAGAGAGGCCCGGGCACCCAGCCCCCCTGAGCGCCCTC 754
| ::||| |||||::: ::|
19 yLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeu..... 33

755 TGAGCTTCATCCCTCGCCACTTCAGACCCCAAGGGAGCAGGCACAACT 804
::: ::| ||:::|
34MetAspSerGlnGlnAlaSerGlyThrIle 43

805 GTCAAGATCGTCCTGAAGGAGAAACATAAG.....AAAGCCTGTGTGCA 848
||:::|||||:::| ||||| | :::::|
44 ValGlnIleValIleAsnAsnLysHisLysHisGlyGlnValCysValse 60

849 TGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCCGCCTTCCGTG 898
:::| ||||| ||||| ||||| ||||| | ::|
60 rAsnGlyLysThrTyrSerHisGlyGluSerTrpHisProAsnLeuArgA 77

FIG. 11

```

899 CCTTCGGCCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAG 948
      ||||| :: |||:|||||:|||||: |||: |||
77  laPheGlyIleValGluCysValLeuCysThrCysAsnValThrLysGln 93

949 GACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTCACCCCGA 998
      ::|||:||||: |||:||||:||||:||||:||||:||||: |||:
94  GluCysLysLysIleHisCysProAsnArgTyrProCysLysTyrProGln 110

999 GAAAGTGGCTGGGAAGTGCTGCAAGATTGCCCCAGAGGACAAAGCAGAC. 1047
      :||||: |||:|||||:||||:||||:||||: |||: |||
110 nLysIleAspGlyLysCysCysLysValCysProGlyLysLysAlaLysG 127

1048 .....CCTGGCCACAGT...GAGATCAGTTCTACCAGGTGTCCCAAG 1086
      |||||:|||| :: :|||: ||| |||
127 luGluLeuProGlyGlnSerPheAspAsnLysGlyTyrPheCysGlyGlu 143

1087 GCACCGGGCGGGTCCTCGTCCACACATCGGTA...TCCCCAAGCCCAGA 1133
      :: |||: |||: |||: |||: |||: |||: |||: |||
144 Glu.....ThrMetProValTyrGluSerValPheMetGluAspGlyGln 158

```

FIG. 11 (CONT.)

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```
1134 CAACCTGCCGCTGCTTTGCCCTGGAACACGAGGCCTCGGACTTGGTGGAGA 1183
      :::: |||:::||||| ||| |||||
158 uThrThrArgLysIleAlaLeuGluThrGluArgProProGlnValGluV 175

1184 TCTACCTCTGGAAGCTGGTAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 1233
      :::::|||| :::
175 alHisValTrpThrIle..... 180

1234 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1283
      |||:::||||| ||
181 .....ArgLysGlyIleLeuGlnHisPheHis.....Il 190

1284 CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGCACAGCACTTCCGAC 1333
      |:::||||::: |||::: ||| |||||:::|
190 eGluLysIleSerLysArgMetPheGlu...GluLeuProHisPheLysL 206
```

FIG. 11 (CONT.²)

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```
256 TTGGTTAAATATCAAGCTGGGTCAAAATGCAAAATCATCAGAAAAGTGG 305
:      |||      :      :      :      :      :      :      :
455 yValVallys.....AspLeuGluProGluLeuLeuArgHisLeuA 469

306 CC.....TTGTTAATTTCAGCAAAG..... 325
      ||      |||||      :      :      :      :      :
469 laLysGlyMetAlaSerLeuLeuIleThrLysGlySerProArgGly 485

326 .....ATTACACATG..... 334
      :      :      :      :      :      :      :
486 GluLeuArgGlyGlnValHisIleAlaAsnGlnCysGluValGlyGlyLe 502

335 .....A 335

502 uArgLeuGluAlaAlaGlyAlaGluGlyValArgAlaLeuGlyAlaProA 519

336 AACCTCATTTCTTCTTCTCCTCCTGCCCCCTCCC.....CCACTGCA.GAA 378
      |||      |||||      :      :      :      :
519 spProAlaSerAlaAlaProProValValProGlyLeuProAlaLeuAla 535
```

FIG. 12 (CONT.¹)

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```

379 CCTCACACTCCCTCTGGACTCCGGGCCCCA.....CCAAAGTCCTGCCA 422
    ||| |||:::|||| ||| |||:::||||
536 ProAlaLysProGlyGlyProGlyArgProArgAspProAsnThrCysPh 552
    :::||| ::: ||||| ::::
423 GCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCCATGAGC 472
    :::||| ::: ||||| ::::
552 ePheGluGlyGlnGlnArgProHisGlyAlaArgTrpAla..... 565
    :::||| ::: ||||| ::::
473 TGTTCCTCCCTCCCGCTGCCCAACCAG.....TGTGTCCTCTGCAGC 513
    ||||| ||| |||||:::
566 .....ProAsnTyrAspProLeuCysSerLeuCysThr 576
    :::||| ::: ||| ::::||||| |||::
514 TGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGAACAGG 563
    ||| ::: ::: ||| ::::||||| |||::
577 CysGlnArgArgThrValIleCysAspProValValCysProProProSe 593
    :||||| |||::: |||||:::||||| :::|||
564 CTGCCCAGCACCCCTCCCGCTGCCAGACTCCTGCTGCCAGGCCCTGCAAAG 613
    :||||| |||::: |||||:::||||| :::|||
593 rCysProHisProValGlnAlaProAspGlnCysCysProValCys.... 608

```

FIG. 12 (CONT.²)

09/890456

```

614 ATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCAT 663
      |||:::||||:::||||
609 .....ProGluLysGlnAspValArgAspLeuPro 618
664 GGGGTGAGACATCCTCAGGATCCA.....TGTTCCAGTGATGCTGG 704
      |||::: ::::| | | | | ||| |||:::
619 GlyLeuProArgSerArgAspProGlyGluGlyCysTyrPheAspGlyAs 635
705 GAGAAAG...AGAGGCCCGGGCACCC.....CCAGCCCCCA 736
      |||::: |||::: | | | | | |||
635 pArgSerTrpArgAlaAlaGlyThrArgTrpHisProValValProProp 652
737 CTGGCCTC.....| | | | | ..... 744
652 heGlyLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGlu 668
745 .....AGCGCCCCCTCT 755
      ::: |||:::
669 valHisCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProVa 685
```

FIG. 12 (CONT.³)

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```

756 GAGCTTCATCCCTCGCCACTTC.....AGACCCAAGGAGCAGGCA 796
      :      |||      |||      |||      |||      |||
685 lArgValAsnProThrAspCysCysLysGlnCysProValGlySerGlyA 702

797 GC...ACAACTGTCAAGATCGTCCCTGAAGGAGAAACATAAGAAAGCCTGT 843
      ::      ::      ::      ::      ::      ::      ::
702 laHisProGlnLeuGlyAspProMetGlnAlaAspGlyProArgGlyCys 718

844 GTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTT 893
      ::|||::      ::      ::      ::      ::      ::      ::
719 ArgPheAlaGlyGlnTrpPheProGluSerGlnSerTrpHisProSerVa 735

894 CCGTGCCCTTCGGCCCCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCC 943
      |||||      ::      |||||      |||      |||      |||
735 lProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyV 752

944 GCCAGGACTGCCAGCGTGTGACCTGTCCCCACCGAGTACCCCTGCCGTCAC 993
      |||:::|||      |||      .      |||      |||
752 alProHisCysGluArgAspAspCysSerLeuProLeuSerCysGlySer 768

```

FIG. 12 (CONT.⁴)

```

994  CCCGAGAAAGTGGCTGGGAAGTCTGCAAGATTGC..... 1029
      :::::      :::::|||||:::  |||
769  GlyLysGlu.....SerArgCysCysSerArgCysThrAlaHisArgAr 783
      1030 .....CCAGAGGACAAAGCAGACCCT 1050
      |||||  :::::|||||
783  gProAlaProGluThrArgThrAspPro 792

```

FIG. 12 (CONT.⁵)

09/890456

486 TGCCTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCCTA 535
||||:||||:||||:||||:||||: |||:||||: |||
691 CysPhePheGluGlyGluGlnHisThrHisGlySerGlnTrpThrProGl 707
536 CT TGAGCCACAAGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGG 585
|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
707 nTyrAsnThr.....CysPheThrCysThrCysGlnLysL 719
586 GCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCCTGTCCACTGCCCC 635
::: ||| ||| ::| ||||| ::: |||
719 ysThr...ValIleCysAspProValMetCysProThrLeuSerCysThr 734
636 CAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTTGGAACCTCA 685
::: ||| ::| ||||| ||||| ||| |||
735 HisThrValGlnProGluAspGlnCysCysProIleCysGluGluLysLy 751
686 CACTCCCTCTGGACTCCGGGCC.....CCACCAAAGT 717
::: ||| . |||: |||: |||: |||: |||: |||: |||: |||: |||:
751 sGluSerLysGluThrAlaAlaValGluLysValGluGluAsnProGluG 768

FIG. 13

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959 GCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGA 1008
851 a.....:..... 851
1009 GAAAGAGAGCCCGGGCACCCCAAGCCCCCACTGGCCTCAGCGCCCTCTG 1058
|||
852AspGlyThr..... 854
1059 AGCTTCATCCCTCGCCACTTCAGACCCCAAGGAGCAGGCAGCAACTGT 1108
854 854
1109 CAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGA 1158
:: ||| ||| :
855ArgLeuCysLysPheGlyLysA 862
1159 AGACGTACTCCCACGGGGAGGTGTGGCACCCCGCCTTCGGTGCCTTCGGC 1208
:: |||:::|||| |||:::
862 snTyrGlnAsnSerGluHisTrpHisProSerValProLeuValGly 878

FIG. 13 (CONT.²)

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```
1209 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCA 1258
      ::: ||||| ||| |||::: ||| |||||
879 GluMetLysCysIleThrCysTrpCysAspHisGlyValThrLysCysG1 895

1259 GCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCGAGAAAGTGG 1308
      |||| | |||| | ||||::: ||| ::::
895 nArgLysGlnCysProLeu...LeuSerCysArgAsnProIleArgThrG 911

      1309 CTGGGAAGTGCTGCAAGATTGCCCCAGAGGAC 1340
          ||||| ||||| ||| |||||
911 luGlyLysCysCysProGluCysIleGluAsp 921
```

FIG. 13 (CONT.³)

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```
932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 981
      :::      ::      |||||
697 .....ProValGlySerGlyAlaHisProG 705

982 AG.....GATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGC 1025
      ||      |||||      :::::|||      |||||
705 InLeuGlyAspProMetGlnAlaAsp.....GlyPro... 715

1026 ACCCCAGCCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCA 1075
715 ..... 715

1076 CTTCAGACCCAAGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGG 1125
715 ..... 715

1126 AGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCACGGG 1175
      :::::|      ::|||:      ::      :::::
716 .....ArgGlyCysArgPheAlaGlyGlnTrpPheProGluSer 728
```

FIG. 14 (CONT.²)

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```

1176 GAGGTGTGGACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCT 1225
      ::: ||||| |||::: ||||| ::: |||||
729 GlnSerTrpHisProSerValProProPheGlyGluMetSerCysIleTh 745

1226 ATGCACCTGTGAGGATGGCCCGCCAGGACTGCCAGCGTGTGACCTGTCCCA 1275
      ||| ||| ||| |||::: ||| |||
745 rCysArgCysGlyAlaGlyValProHisCysGluArgAspAspCysSerL 762

1276 CCGAGTACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAG 1325
      ||| ::::: ::::: |||||:::
762 euProLeuSerCysGlySerGlyLysGlu.....SerArgCysCysSer 776

1326 ATTTGC.....CCAGAGGACAAAGCAGACCCCT 1352
      ||| ||||| ::::: |||||
777 ArgCysThrAlaHisArgArgProAlaProGluThrArgThrAspPro 792

```

FIG. 14 (CONT.³)

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```
243 GAGACAGTGGCATGCCCAGTGTTCACAGTAAGTGTGTGTAAGCCGAG 292
   :: ||| |||||::: ||| ::|||::: |||::
724 AspProValMetCysProThrLeuSerCysThrHisThrValGlnProGln 740

293 ATTCAAACCTCAGACCTTCTGGCCCCCTTGCCCTAGGAGAGCATGCCCCAGTTG 342
   : ::::: |||||:::
740 u.....AspGlnCysCysProIle. 746

343 TCTAGCAGATTCTCTTTTGCCCTGAGTGGCCAGATGACATCTCTTTTAGA 392
   +++ ||| ::: ::::: :::
747 .....CysGluGluLysLysGluSerLysGluThrAla 757

393 GCTAGAAAGAGGAGAAATGAGACAGGGTCTTTGGGCTGGAGCCTCCTGG 442
   ||| ::||| ::::++ ::||| ||
758 AlaValGluLysValGlu.....GluAsnProGluGln 768

443 GACTAACATGGCACTGGTCGGTTTGCCAGGCCCCAGACATGTTCTGCCCTTT 492
   | ||| |
768 y.....CysTyrP 771

493 TCCATGGG.....AAGAGATACTCCCCCGCGGAGAGCTGGCACCCCTAC 536
   ||::||| ||| ::::: ||||| ::||| |||||:::
771 heGluGlyAspGlnLysMetHisAlaProGlyThrThrTrpHisProphe 787
```

FIG. 15

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```

537 TTGGAGCCACAAGGCCTGATGTACTGCCCTGCGCTGTACCTGC...TCAGA 583
    ::  |||  |||  ::  |||  |||||  ::::
788 ValProProPheGlyTyrIleLysCysAlaValCysThrCysLysGlySe 804

584 GGGCGCCCATGTGAGTTGTACCGCCTCCACTGTCCGCCTGTCCACTGCC 633
    :  :::::| | |  |||  :::::  |||||  :::  |||
804 rThrGlyGluValHisCysGluLysValThrCysProProLeuThrCysS 821

634 CCCAGCCTGTG...ACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAA 680
    ::|||:::  ::|||:::| | |  |||  :::| | |
821 erArgProIleArgArgAsnProSerAspCysCysLysGluCysProPro 837

681 CCTCACACTCCC.....TCTGGACT 700
    ::||| | | |
838 GluGluThrProProLeuGluAspGluGluMetMetGlnAlaAspGlyTh 854

701 CCGGGCCCCACCAAGTCCTGCCAGCACACAACGGGACCATGTACCAACACG 750
    |||  |||:::  :::  :::  |||||  ::::
854 rArgLeu.....CysLysPheGlyLysAsnTyrTyrGlnAsnS 867

751 GAGAGATCTTCAGTGCCCATGAGCTGTTCCTCCCTCCCGCCTGCCCAACCAG 800
    ::|||  :::  |||  |||  :::
867 erGluHisTrp.....HisProSerValProLeuValGlyGluMetLys 881

```

FIG. 15 (CONT.¹)

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801 TGTGTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCCTCACAAC 850
|||::: ||| ||| :::||| |||
882 CysIleThrCysTrpCysAspHisGlyValThrLysCysGlnArgLysG1 898
851 CTGCCCCGAACAGGCTGCCCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
||||| :::||| |||::: :::|||
898 nCysProLeuSerCysArgAsnProIleArgThrGluGlyLysCysC 915
901 GCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGT 950
|| ||| ::::: |||:::~::~:
915 ysProGluCysIleGluAspPheMetGluLysGluMetAlaLysMet 931
951 GTGCAGTCGCTCCATGGGGTGAGACAT 977
:::~::~: ::| |||||
932 AlaGluLysLysLysSerTrpArgHis 940

FIG. 15 (CONT.²)

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462 GGTTCGCCAGGCCAGACATGTTCTGCCTTTTCCATGGGAAGAGATACTC 511
 ||| ||| |||:::||||:::||||:::|
 543 GlyArgProArgAspProAsnThrCysPheGluGlyGlnGlnArgPr 559
 512 CCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCCTGATGTACT 561
 ||| ||| ||| ::||| |
 559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.....LeuC 572
 562 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 611
 || |||||::: :: ||| ||| :::
 572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587
 612 CACTGTCCGCGCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG 661
 ||||| |||||:::||||| |||:::|||||
 588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604
 662 CTGTCCCAAGTGTGTGAA.....CCTCACACTC 690
 ||||| ||| ||| . ||| |
 604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621

FIG. 16

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```

691 CCTCTGGACTCCGGGCCCCACCAAGTCTCTGCCAGCACAAACGGGACCATG 740
    || :::: ||| ||| ::::: ||| :::: |||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636

741 TACCAACACGGAGAGATCTTCAGTGCCCAATGAGCTGTTCCCCCTCCCGCCT 790
    ::::: ||| ||| :::: |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProPropheGl 653
    ::::: ||| ||| :::: |||

791 GCCCAACCAGTGTGTCCTCTGCAGCTGCACA.....GAGGGCCAGATCT 834
    ::: ||| ::::: ||| ::::: |||
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670

835 ACTGGGGCCTCACAACTGCCCCCGAACCAGGCTGCCCCAGCACCCCTCCCG 884
    ::: ||| :::: ||| ||| :::: |||
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686

885 CTG...CCAGACTCCTGTGCTGCCAAGCCTGCAAGATGAGGCAAGTGAGCA 931
    ::: ||| :::: ||| ||| :::: |||
687 ValAsnProThrAspCysCysLysGlnCys..... 696

```

FIG. 16 (CONT.¹)

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932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTGAGACATCCTC 981
 ::: ::: |||||
697ProValGlySerGlyAlaHisProG 705

982 AG.....GATCCATGTTCCAGTGATGCTGGGAGA 1010
 || ||||| ::: |||
705 InLeuGlyAspProMetGlnAlaAspGlyProArg 716

FIG. 16 (CONT.²)

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```

243 GAGACAGTGGCATGCCAGTGTTCACACAGTAAGTGTGGTAAAGCCGAG 292
   :::   |||   |||||:::| | |   ::|||:::| | |::
724 AspProValMetCysProThrLeuSerCysThrHisThrValGlnProG1 740

293 ATTCAAACCTCAGACCTTCTGGCCCCCTTGCCTAGGAGAGCATGCCCAGTGT 342
   :
740 u.....AspGlnCysCysProIle. 746

343 TCTAGCAGATTCTCTTTTGCCTGAGTGGCCCCAGATGACATCTCTTTAGA 392
   +++   |||   ::   :::::   ::
747 .....CysGluGluLysLysGluSerLysGluThrAla 757

393 GCTAGAAAGAGGAGAAATGAGACAGGGTCTTTGGGCTGGAGCCTCCTGG 442
   |||   ::|||   ::+++   ::|||   ||
758 AlaValGluLysValGlu.....GluAsnProGluG1 768

443 GACTAACATGGCACTGGTCGGTTTGCCAGGCCCCAGACATGTCTGCCTTT 492
   |
768 Y.....CysTyrP 771

```

FIG. 17

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```

493 TCCATGGG.....AAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTAC 536
    ||:::||||   |||   :::::|||||   :::|||||:::
771 heGluGlyAspGlnLysMetHisAlaProGlyThrThrTrpHisProPhe 787

537 TTGGAGCCCAAGGCCTGATGTACTGCCTGCGCTGTACCTGC...TCAGA 583
    ::   |||   |||   ::   |||   |||||   ::::
788 ValProProPheGlyTyrIleLysCysAlaValCysThrCysLysGlySe 804

584 GGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCCTGTCCACTGCC 633
    :   :::::||||   |||   :::::   |||||:::   |||
804 rThrGlyGluValHisCysGluLysValThrCysProProLeuThrCysS 821

634 CCCAGCCTGTG...ACGGAGCCACAGCAATGCTGTCCCAAGTGTGGAA 680
    :::||||:::   :::||||:::|||||   :::||||
821 erArgProIleArgArgAsnProSerAspCysCysLysGluCysProPro 837

681 CCTCACACTCCC.....TCTGGACT 700
    :::|||||
838 GluGluThrProProLeuGluAspGluGluMetMetGlnAlaAspGlyTh 854

```

FIG. 17 (CONT.¹)

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```
701 CCGGGCCCAACCAAGTCTGCCAGCACAAACGGACCATGTACCAACAG 750
    |||
    |||::: ::: |||:::
854 rArgLeu.....CysLysPheGlyLysAsnTyrTyrGlnAsnS 867
751 GAGAGATCTTCAGTGCCCATGAGCTGTTCCTCCCTCCCGCTGCCCAACCAG 800
    ::||| ::: ||| ||| :::
867 erGluHisTrp.....HisProSerValProLeuValGlyGluMetLys 881
801 TGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCTCACAAC 850
    |||::: ||| ||| ::||| |||
882 CysIleThrCysTrpCysAspHisGlyValThrLysCysGlnArgLysG1 898
851 CTGCCCCGAACCAGGCTGCCCCAGCACCCCTCCCGCTGCCAGACTCCTGCT 900
    ||||| ::||| |||::: |||:::
898 nCysProLeuLeuSerCysArgAsnProIleArgThrGluGlyLysCysC 915
901 GCCAAGCCTGCAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGT 950
    || ||| ::::: |||:::
915 ysProGluCysIleGluAspPheMetGluLysGluGluMetAlaLysMet 931

951 GTGCAGTCGCTCCATGGGGTGAGACAT 977
    ::::: :: |||||
932 AlaGluLysLysLysSerTrpArgHis 940
```

FIG. 17 (CONT.²)

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```

462 GGTTCAGGCCGACATGTTCTGCCTTTCATGGGAAGAGATACTC 511
      |||   |||           |||:::|||:::|||:::|||:::|||:::
543 GlyArgProArgAspProAsnThrCysPhePheGluGlyGlnGlnArgPr 559
      |||   |||   |||   |||   ::|||   |
512 CCCCCGGAGAGCTGGCACCCCTACTTGAGGCCACAAGGCCTGATGTACT 561
      |||   |||   |||   |||   ::|||   |
559 oHisGlyAlaArgTrpAlaProAsnTyrAspPro.....LeuC 572
      |||   |||   |||   |||   |||   |||   |||   |||   |||
562 GCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTC 611
      ||   |||||||||:::  ::  |||   |||   ::
572 ysSerLeuCysThrCysGlnArgArgThr...ValIleCysAspProVal 587
      |||   |||   |||   |||   |||   |||   |||   |||   |||
612 CACTGTCCGCTGTCCACTGCCCCCAGCCCTGTGACGGAGCCACAGCAATG 661
      |||||||||   ||||||::|  |||||   |||::|  |||||
588 ValCysProProProSerCysProHisProValGlnAlaProAspGlnCy 604
      |||   |||   |||   |||   .       |||   |
662 CTGTCCCAGTGTGTGGAA.....CCTCACACTC 690
      |||||||   |||   |||   |||   .       |||   |
604 sCysProValCysProGluLysGlnAspValArgAspLeuProGlyLeuP 621

```

FIG. 18

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691 CCTCTGGACTCCGGGCCCCACCAAGTCCTGCCAGCACAAACGGGACCATG 740
|| :::: ||| ||| ::::: ||| :::: |||
621 roArgSer...ArgAspProGlyGluGlyCysTyrPheAspGlyAspArg 636
741 TACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCT 790
::::: ||| :::: |||
637 SerTrpArgAlaAlaGlyThrArgTrpHisProValValProProPheG1 653
791 GCCCAACCAGTGTCTCTCTGCAGCTGCACA.....GAGGGCCAGATCT 834
::::: ||| :::: ||| ||| ::::: |||
653 yLeuIleLysCysAlaValCysThrCysLysGlyGlyThrGlyGluValH 670
835 ACTGCGGCCTCACAACTGCCCCCGAACCAGGCTGCCAGCACCCCTCCCG 884
::::: ||| :::: ||| ::::: ||| ||| ::::
670 isCysGluLysValGlnCysProArgLeuAlaCysAlaGlnProValArg 686
885 CTG...CCAGACTCCTGCTGCCAAGCCTGCAAGATGAGGCAAGTGAGCA 931
:::: ||| :::: ||| ::::: |||
687 ValAsnProThrAspCysCysLysGlnCys..... 696

FIG. 18 (CONT.¹)

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```
932 ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTC 981
    ::: ::: |||||
697 .....ProValGlySerGlyAlaHisProG 705

982 AG.....GATCCATGTTCCAGTGATGCTGGGAGA 1010
    || ||||| :::::||||: |||
705 lnLeuGlyAspProMetGlnAlaAspGlyProArg 716
```

FIG. 18 (CONT.²)

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FIG. 19

[illegible]

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rdinLM_var1 181
 rdinLM_var2 181
 rdinLM_var4 75
 rdinLM_var5 75
 rdinLM_var3 22
 rdinLM_var6 75

rdinLM_var1 239
 rdinLM_var2 239
 rdinLM_var4 133
 rdinLM_var5 133
 rdinLM_var3 82
 rdinLM_var6 133

rdinLM_var1 299
 rdinLM_var2 299
 rdinLM_var4 193
 rdinLM_var5 193
 rdinLM_var3 142
 rdinLM_var6 193

FIG. 19 (CONT.¹)

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```

dinLM_var1 359 [REDACTED]
dinLM_var2 359 [REDACTED]
dinLM_var4 253 [REDACTED]
dinLM_var5 243 [REDACTED]
dinLM_var3 202 [REDACTED]
dinLM_var6 243 [REDACTED]

```

```

dinLM_var1 419 [REDACTED]
dinLM_var2 419 [REDACTED]
dinLM_var4 313 [REDACTED]
dinLM_var5 248 [REDACTED]
dinLM_var3 262 [REDACTED]
dinLM_var6 248 [REDACTED]

```

```

rdinLM_var1 472 [REDACTED]
rdinLM_var2 472 [REDACTED]
rdinLM_var4 366 [REDACTED]
rdinLM_var5 301 [REDACTED]
rdinLM_var3 315 [REDACTED]
rdinLM_var6 308 IKKVRKQ [REDACTED] FOK [REDACTED] ERLIA [REDACTED] EGHM [REDACTED] F AQTL LKVTAS [REDACTED] DKV [REDACTED] KT*~~~~~

```

FIG. 19 (CONT.²)

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chordinLM_var1	524	* ERLPSFPRRREGHGRRRQSTOPTNT	*
chordinLM_var2	524	ERLPSFPRRREGHGRRRQSTOPTNT	*
chordinLM_var4	418	ERLPSFPRRREGHGRRRQSTOPTNT	*
chordinLM_var5	353	ERLPSFPRRREGHGRRRQSTOPTNT	*
chordinLM_var3	367	ERLPSFPRRREGHGRRRQSTOPTNT	*
chordinLM_var6	357	~~~~~	~

FIG. 19 (CONT.³)

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425 AGACATTCC.....CAGGATCCATGCTCGGAGAGGAGAGG 459
|||||
1 ArgHisSerTyrHisArgSerHisTyrAspProProSerArgGlnAl 17
460 CCCCAGCAGCCAGCCCCCACCAGCCTCAGCTCCCCCTCTGGGCTTCATCC 509
: : : : :
17 aGlyGlyLeuSerArgPheProGlyAlaArgSerHisArgGlyAlaLeuM 34
510 NTCGCCACTTCCAGTCAGTAGGAATGGGCAGCACAAACCATCAAGATTATC 559
||| : : : : :
34 etAspSerGlnGlnAlaSerGly.....ThrIleValGlnIleVal 47
560 TTGAAGGAGAAACATAAA.....AAAGCTTGACACACAATGGGAAGAC 603
: : : : :
48 IleAsnAsnLysHisLysHisGlyGlnValCysValSerAsnGlyLysTh 64
604 ATACTCCCATGGGGAGGTGTGGCACCCCACTGTGCTCTCCTTTGGCCCCCA 653
|||||
64 rTyrSerHisGlyGluSerTrpHisProAsnLeuArgAlaPheGlyIleV 81

FIG. 20

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```
862 ATCTCCAAGCCAGACAGCCTACACCGCTTGTCTCTGGAGCATGAAGCCT 911
    :::          :::::      :::::|||||  |||
153 eMetGluAspGlyGluThrThrArgLysIleAlaLeuGluThrGluArgP 170

912 CTGACCAGGTAGAGATGTACATTTGGAAGCTGGTGAAAGGAATTTACCAC 961
    |||||||:::~::~~::  |||||||  :::
170 roProGlnValGluValHisValTrpThrIleArgLysGlyIleLeuGln 186

962 TTGGTTCAGATCAAGAGAGTCAGGAAGCAAGATTTCAGAAAGAGGTTCA 1011
    ::|||:::~::~~::  |||::  |||:::
187 HisPheHisIleGluLysIleSerLysArgMetPheGlu...GluLeuPr 202

1012 GAACTTCCGGCTGCTCACCGGCACCCATGAAGGTTACTGGACCGTTTCC 1061
    ::|||:::|||||  |||  ::  |||  :::|||
202 oHisPheLysLeuValThrArgThrThrLeuSerGlnTrpLysIlePheT 219

1062 TA.....GCCCAGATTCCAGAGCTGAAAGTTACAGCCAGCCACGAC 1102
    |||||||  :::::
219 hrGluGlyGluAlaGlnIleSerGlnMet.....CysSerSer 231
```

FIG. 20 (CONT.²)

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```
1103 AAAGTGACCAAGACATTATAGCAAGGACCCTAAAGAGTTGCAGATACGAGT 1152
      ::|||  ::|||  +++      |||||::
232 ArgValCysArgThr.....GluLeuGluAsp..... 240

1153 TTTATTGGTTTGTGTTATTATATATAATTAATAA 1183
      |||||  ::|||:::~::~:
241 ....LeuValLysValLeuTyrLeuGluArg 249
```

FIG. 20 (CONT.³)

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18 CCCACACTGCTCTGCCCTACCCACACCA...GCCCCAAGGTCTNAGAAAGC 64
||| ||| ::: ||| ||| ||||| :::|||
673 ProMetLeuProAlaGlyProGlyProGluAlaProValProAlaLysHi 689

65 CCTGGAGGCTGGCTTGCCA...AATCCCTTGTCAGTGTNTTATTGATTAG 111
::: ||| ||| :::||| ||| :::+++
689 sGlySerProGlyArgProArgAspProAsnThrCysPhe..... 703

112 TCTGAGAATATCTTAGACCTCACCCACAAGTTCTGTGTGGAGC..... 155
+++ ::: |||:::||||::: |||:::
704GluGlyGlnGlnArgProHisGlyAlaArgTrpAlaProAsn 717

156CTGTGCTCTCTGTCTGTGT.....CTGTCTGTCTG 187
||||||| ||| :::||| :::||
718 TyrAspProLeuCysSerLeuCysIleCysGlnArgArgThrValIleCy 734

188 TCTGTCTGTCTGTGCCCTGCCCTCTCTCTGTCTGTCTGCCGTCTGTCTCTG 237
| ||| ||| . ||| |||
734 sAspProValValCysProProProSerCysProHisPro..... 747

FIG. 21

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238 TCTCTGTGTCTCTGTCTG.TCTCTTTCTCTCTGTCTCTCTGTGT 286
||| ::|||::: ||| :::|||
748ValGlnAlaLeuAspGlnCysCysProValCys 758
287 CTCTGTCTCTGTCTCTCTCTCTCTCTCTCAGAAAGTCCTCTAGCCTT 336
|||
759ProGluLysG1 762
337 CTCTAGCAGGCGTCTC.....ATGCAGCCTGGT...TGGT 368
||||| ||| :::::||||| |
762 nArgSerArgAspLeuProSerLeuProAsnLeuGluProGlyGluGlyC 779
369 GT.....TCCCAGCTGTGGCCTATCCCACAGACAGCTCCACAT 406
|| ::::: ||| |||
779 yTyrPheAspGlyAspArgSerTrpArgAlaAlaGlyThrArgTrpHis 795
407 CCT.....GCTTGCTGTTC 420
||| ::: |||:::
796 ProValValProPheGlyLeuIleLysCysAlaValCysThrCysLy 812

FIG. 21 (CONT.¹)

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```

421 GCAGAGACATTCCCAGGATCCATGCTCGGAGAGGAGAGGCCCC..... 463
      :          :      :      :      :      :      :      :
812 sGlyAlaThrGlyGluValHisCysGluLysValGlnCysProArgLeuA 829
      :          :      :      :      :      :      :      :
464 .....AGCAGCCAGCCGCCCCACCCAGCCTCAGCTCC 493
      :      :      :      :      :      :      :      :
829 laCysAlaGlnProValArgAlaAsnProThrAspCysCysLysGlnCys 845
      :          :      :      :      :      :      :      :
494 CCTCTGGGCTTCATCCNTCGCCACTTCCAGTCAGTAGGAATGGGCAGCAC 543
      :      :      :      :      :      :      :      :
846 ProValGly.....SerGlyTh 851
      :          :      :      :      :      :      :      :
544 AACCATCAAGATT.....ATCTTGAAGGAGAAACATAAAAAAGCTTGCA 587
      :      :      :      :      :      :      :      :
851 rAsnAlaLysLeuGlyAspProMetGlnAlaAspGlyProArgGlyCysA 868
      :          :      :      :      :      :      :      :
588 CACACAAATGGGAAGACATACTCCCATGGGGAGGTGTGGCACCCCACTGTG 637
      :      :      :      :      :      :      :      :
868 rgPheAlaGlyGlnTrpPheProGluAsnGlnSerTrpHisProSerVal 884
      :          :      :      :      :      :      :      :

```

FIG. 21 (CONT.²)

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```

638 CTCTCCTTTGGCCCCCATGCCCTGCATCCTGTGCACATGTATTGATGGCTA 687
      ||||| ||| ||||| ||| ||| |||
885 ProProPheGlyGluMetSerCysIleThrCysArgCysGlyAlaGlyVa 901

688 CCAGGACTGCCACCGTGTGACCTGCCCCACCCCAATATCCCTGCAGTCAAC 737
      |||:::|||| ||| |||:::~::~
901 lProHisCysGluArgAspAspCysSerProProLeuSerCysGlySerG 918

738 CCAAGAAAGTGGCTGGGAAGTGTGCAAGATCTGC..... 772
      |||::: |||::: |||::: |||::: |||
918 lYlysGlu.....SerArgCysCysSerHisCysThrAlaGlnArgSer 932

773 .....CCAGAGGACGAGCGGGAAGATGACCACAGT 802
      ||||| ||| ||| ::|||
933 SerGluThrArgThrLeuProGluLeuGluLysGluAlaGluHisSer 948

```

FIG. 21 (CONT.³)

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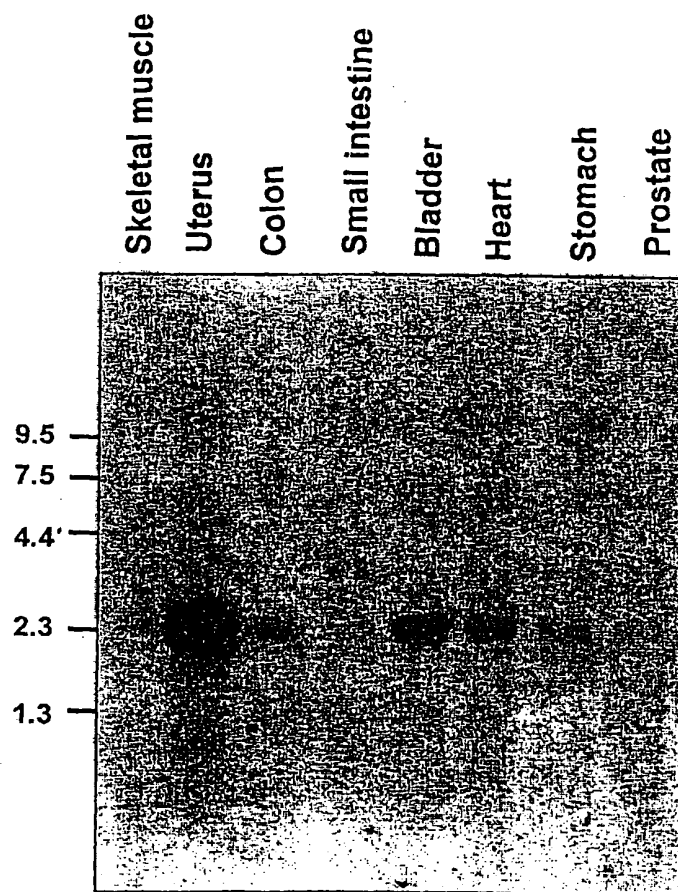


Fig. 22

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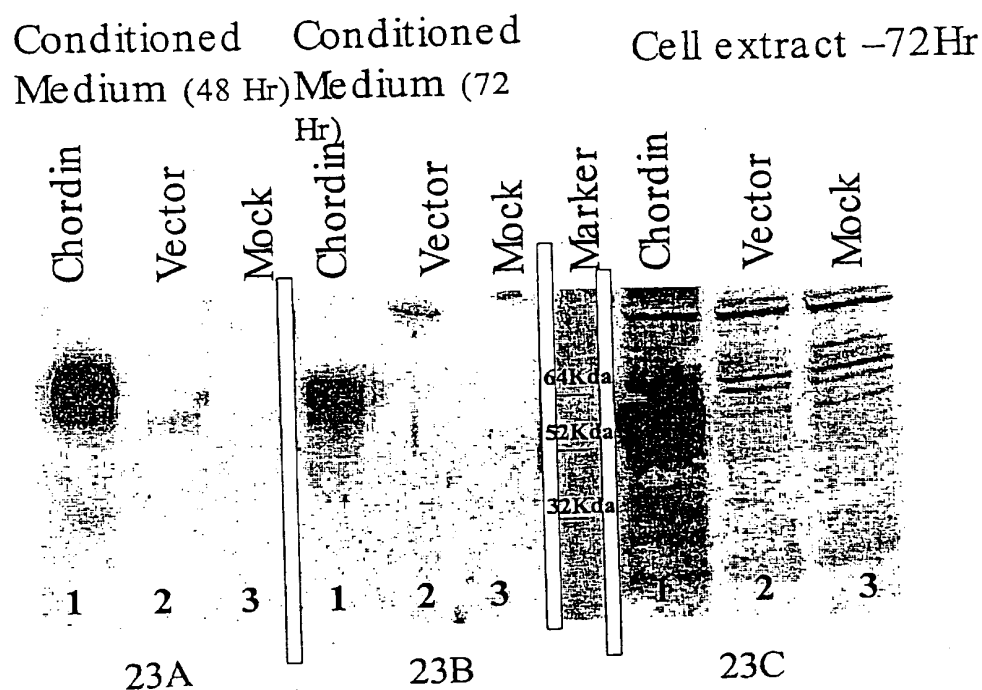


Fig. 23

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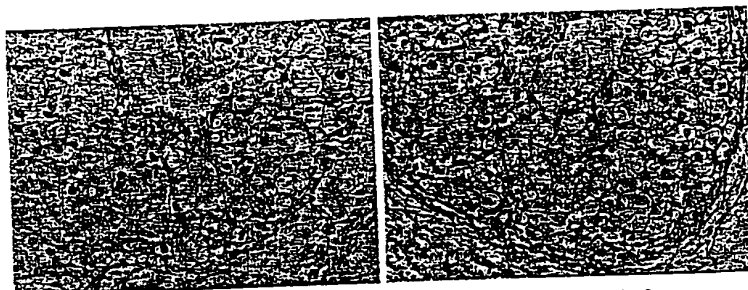


Fig.24A

Fig.24A'



Fig.24B

Fig.24B'

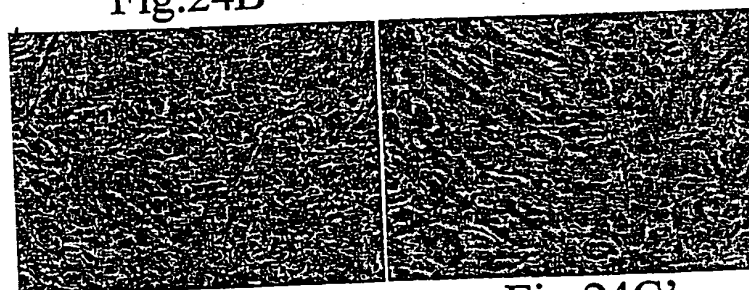


Fig.24C

Fig.24C'

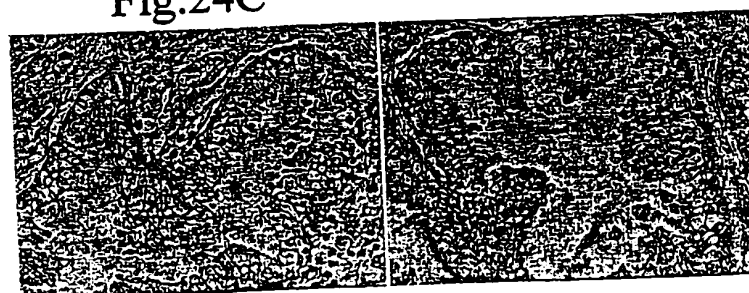


Fig.24D

Fig.24D'

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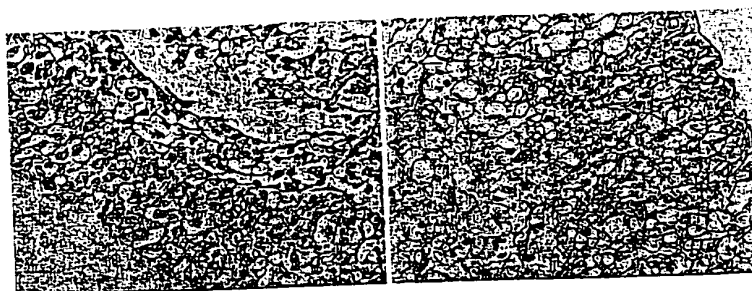


Fig.24E

Fig.24E'

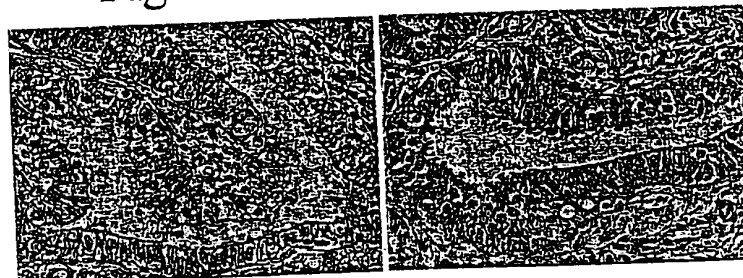


Fig.24F

Fig.24F'

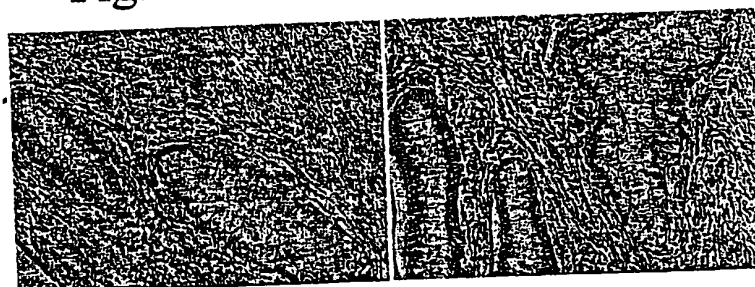


Fig.24G

Fig.24G'

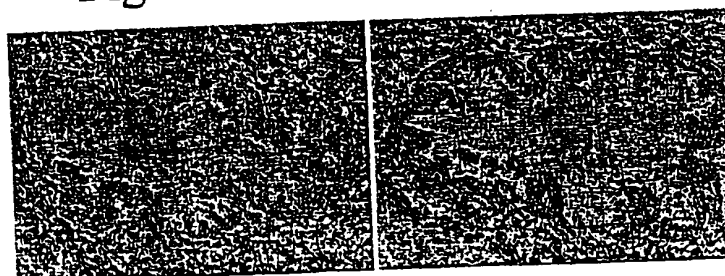


Fig.24H

Fig.24H'

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Fig.24I

Fig.24I'

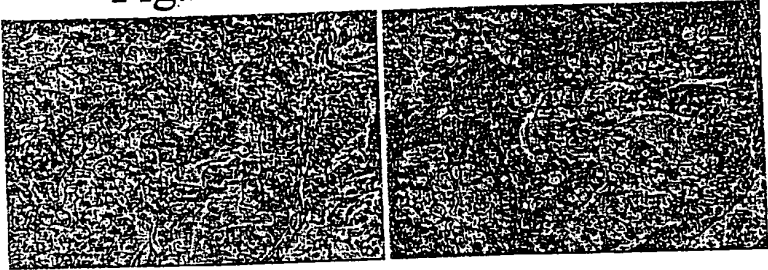


Fig.24J

Fig.24J'

Osteoblasts

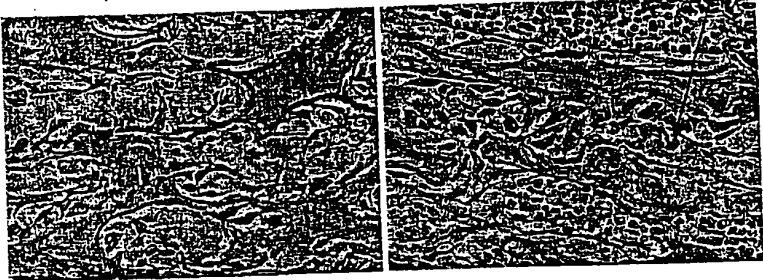
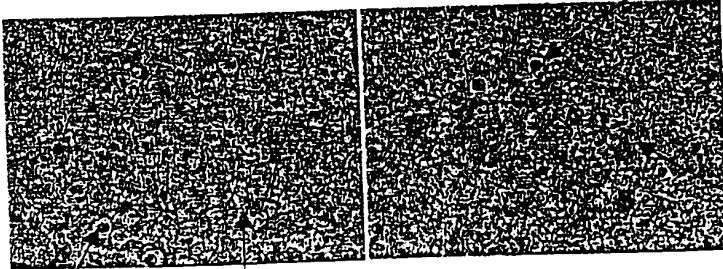


Fig.24K

Fig.24K'

Oligodendroglia



Oligodendroglia

Gemistocyte

Gemistocyte
(activated
astrocyte)

Fig.24L

Fig.24L'

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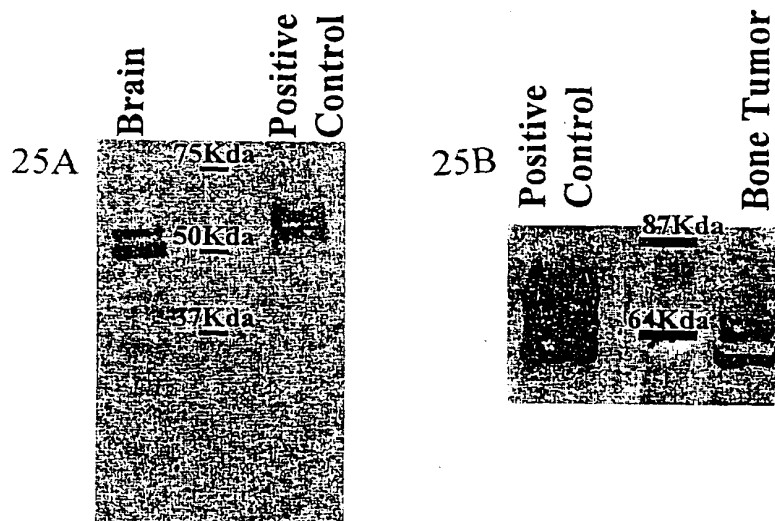


Fig. 25